

APPENDIX A (Sequence alignment)

RESULT 1

PAK2_HUMAN

ID PAK2_HUMAN STANDARD; PRT; 524 AA.

AC Q13177; Q13154;

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated kinase 2) (PAK-2) (PAK65) (Gamma-PAK) (S6/H4 kinase).

GN PAK2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Sells M., Knause U.J., Bagrodia S., Ambrose D., Bokoch G.M., Chernoff J.;

RL Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 32-524 FROM N.A., AND SEQUENCE OF 401-417.

RC TISSUE=Placenta;

RX MEDLINE=95262637; PubMed=7744004;

RA Martin G.A., Bollag G., McCormick F., Abo A.;

RT "A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation is related to PAK65 and STE20.";

RL EMBO J. 14:1970-1978(1995).

RN [3]

RP ERRATUM.

RX MEDLINE=96016211; PubMed=7556080;

RA Martin G.A., Bollag G., McCormick F., Abo A.;

RL EMBO J. 14:4385-4385(1995).

RN [4]

RP AUTOPHOSPHORYLATION.

RX MEDLINE=95403344; PubMed=7673144;

RA Benner G.E., Dennis P.B., Masaracchia R.A.;

RT "Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular and intermolecular autophosphorylation.";

RL J. Biol. Chem. 270:21121-21128(1995).

CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS. PHOSPHORYLATES RIBOSOMAL PROTEIN S6, HISTONE H4 AND MYELIN BASIC PROTEIN.

CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1.

CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HIGHER LEVELS SEEN IN SKELETAL MUSCLE, OVARY, THYMUS AND SPLEEN.

CC -!- PTM: Autophosphorylated when activated by CDC42/p21.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. STE20 subfamily.

CC -!- SIMILARITY: Contains 1 CRIB domain.

CC -----

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CC -----

DR EMBL; U24153; AAA65442.1; -.

DR EMBL; U25975; AAA75468.1; -.

DR PIR; S58682; S58682.

DR HSSP; P24941; 1CKP.

DR Genew; HGNC:8591; PAK2.

DR MIM; 605022; -.

DR GO; GO:0004672; F:protein kinase activity; TAS.

DR GO; GO:0006469; P:negative regulation of protein kinase activity; TAS.

DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR000095; PAKbox/Rhobndng.

DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 74 87 CRIB.
 FT DOMAIN 88 248 LINKER.
 FT DOMAIN 249 499 PROTEIN KINASE.
 FT NP_BIND 255 263 ATP (BY SIMILARITY).
 FT BINDING 278 278 ATP (BY SIMILARITY).
 FT ACT_SITE 367 367 BY SIMILARITY.
 FT CONFLICT 90 90 A -> T (IN REF. 2).
 FT CONFLICT 150 150 L -> F (IN REF. 2).
 FT CONFLICT 225 225 P -> T (IN REF. 2).
 FT CONFLICT 329 329 G -> R (IN REF. 2).
 FT CONFLICT 338 338 T -> TA (IN REF. 1).
 SQ SEQUENCE 524 AA; 58004 MW; DB2A7A72BE6B1072 CRC64;

Query Match 100.0%; Score 2707; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.3e-142;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDNGELEDKPPAPPVRMSSTIFSTGGKDPLSANHSLKPLPSVPPEKKPRHKIISIFSGT 60
 |||||
 Db 1 MSDNGELEDKPPAPPVRMSSTIFSTGGKDPLSANHSLKPLPSVPPEKKPRHKIISIFSGT 60
 |||||
 Qy 61 EKGSKKKEKERPEISPPSDFEHTIHVGFDVAVTGEFTGMPEQWARLLQTSNITKLEQKKNP 120
 |||||
 Db 61 EKGSKKKEKERPEISPPSDFEHTIHVGFDVAVTGEFTGMPEQWARLLQTSNITKLEQKKNP 120
 |||||
 Qy 121 QAVLDVLKFYDSNTVKQKYLSTPPEKDGLPSGTPALNAKGTEAPAVVTEEDDDEETAP 180
 |||||
 Db 121 QAVLDVLKFYDSNTVKQKYLSTPPEKDGLPSGTPALNAKGTEAPAVVTEEDDDEETAP 180
 |||||
 Qy 181 PVIAPRPDHTKSIYTRSVIDPVPAPVGDSHVDGAAKSLDKQKKPKMTDEEIMEKLRTIV 240
 |||||
 Db 181 PVIAPRPDHTKSIYTRSVIDPVPAPVGDSHVDGAAKSLDKQKKPKMTDEEIMEKLRTIV 240
 |||||
 Qy 241 SIGDPKKKYTRYEKIGQGASGTVFTATDVALGQEVAIKQINLQKQPKKELINEILVMKE 300
 |||||
 Db 241 SIGDPKKKYTRYEKIGQGASGTVFTATDVALGQEVAIKQINLQKQPKKELINEILVMKE 300
 |||||
 Qy 301 LKNPNIVNFLDSYLVGDELFFVMEYLAGGSLTDVVTETCMDEAQIAAVCRECLQALEFLH 360
 |||||
 Db 301 LKNPNIVNFLDSYLVGDELFFVMEYLAGGSLTDVVTETCMDEAQIAAVCRECLQALEFLH 360
 |||||
 Qy 361 ANQVIHRDIKSDNVLLGMEGSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAY 420
 |||||
 Db 361 ANQVIHRDIKSDNVLLGMEGSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAY 420
 |||||
 Qy 421 GPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPEKLSPIFRDFLNRC 480
 |||||
 Db 421 GPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPEKLSPIFRDFLNRC 480
 |||||
 Qy 481 LEMDVEKRGSAKELLQHPFLKLAKPLSSLTPLIMAAKEAMKSNR 524
 |||||
 Db 481 LEMDVEKRGSAKELLQHPFLKLAKPLSSLTPLIMAAKEAMKSNR 524
 |||||